

# SCORE Search Results Details for Application 10568337 and Search Result 20071129\_084935\_20071129\_084935\_us-10- 568-337-2.p2n.rni.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10568337 and Search Result 20071129\_084935\_20071129\_084935\_us-10-568-337-2.p2n.rni.

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GenCore version 6.2.1  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 29, 2007, 08:49:46 ; Search time 836 Seconds  
(without alignments)  
120.985 Million cell updates/sec

Title: US-10-568-337-2  
Perfect score: 124  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310228

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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- 9: /EMC\_Celerra\_SIDS2/ptodata/1/ina/PP\_COMB.seq:\*
- 10: /EMC\_Celerra\_SIDS2/ptodata/1/ina/RE\_COMB.seq:\*
- 11: /EMC\_Celerra\_SIDS2/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	124	100.0	2163	2	US-07-731-157A-1	Sequence 1, Appli
2	124	100.0	2163	2	US-08-541-780-1	Sequence 1, Appli
3	55	44.4	36	2	US-07-731-157A-11	Sequence 11, Appl
4	55	44.4	36	2	US-08-541-780-11	Sequence 11, Appl
c 5	54	43.5	531	5	US-10-703-032-95089	Sequence 95089, A
c 6	54	43.5	539	5	US-10-703-032-91504	Sequence 91504, A
c 7	54	43.5	588	5	US-10-703-032-94706	Sequence 94706, A
c 8	53	42.7	419	5	US-10-703-032-49153	Sequence 49153, A
c 9	52.5	42.3	378	5	US-10-703-032-89469	Sequence 89469, A
c 10	52.5	42.3	396	5	US-10-703-032-98346	Sequence 98346, A
c 11	52.5	42.3	418	5	US-10-703-032-98096	Sequence 98096, A
c 12	52.5	42.3	422	5	US-10-703-032-96699	Sequence 96699, A
c 13	52.5	42.3	425	5	US-10-703-032-97933	Sequence 97933, A
c 14	52.5	42.3	428	5	US-10-703-032-80385	Sequence 80385, A
c 15	52.5	42.3	433	5	US-10-703-032-80412	Sequence 80412, A
c 16	52.5	42.3	438	5	US-10-703-032-49995	Sequence 49995, A
c 17	52.5	42.3	473	5	US-10-703-032-92026	Sequence 92026, A
c 18	52.5	42.3	475	5	US-10-703-032-55226	Sequence 55226, A

&lt;!--StartFragment--&gt;

## ALIGNMENTS

## RESULT 1

US-07-731-157A-1

; Sequence 1, Application US/07731157A

; Patent No. 5457032

## ; GENERAL INFORMATION:

; APPLICANT: Quax, Wilhelmus J.

; APPLICANT: Misset, Onno

; APPLICANT: Van der Laan, Jan M.

; APPLICANT: Lenting, Herman B.M.

; TITLE OF INVENTION: Mutated beta-lactam acylase genes

; NUMBER OF SEQUENCES: 50

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON &amp; TATUM

; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94306

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

## ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/731,157A

; FILING DATE: 19910509

; CLASSIFICATION: 435

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 90200962

; FILING DATE: 18-APR-1990

## ; ATTORNEY/AGENT INFORMATION:

; NAME: RAE-VENTER PH.D., BARBARA

; REGISTRATION NUMBER: 32,750

; REFERENCE/DOCKET NUMBER: GBRO-027/00US

## ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-494-7622

; TELEFAX: 415-857-0663

; TELEX: 380816 COOLEY PA

## ; INFORMATION FOR SEQ ID NO: 1:

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 2163 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

## ; ORIGINAL SOURCE:

; ORGANISM: Pseudomonas species

; STRAIN: SY77

## ; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..2163

; IDENTIFICATION METHOD: experimental

; OTHER INFORMATION: /codon\_start= 1

; OTHER INFORMATION: /product= "Glutaryl-Cef acylase"

; OTHER INFORMATION: /evidence= EXPERIMENTAL

## ; FEATURE:

; NAME/KEY: sig\_peptide

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US-07-731-157A-1

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Query Match:	100.0%	Indels:	0
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US-10-568-337-2 (1-27) x US-07-731-157A-1 (1-2163)

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Qy      21 AlaProAlaValAlaPheAla 27
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Db      61 GCGCCCGCCGTCGCCTTTGCG 81

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## RESULT 2

US-08-541-780-1

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; Sequence 1, Application US/08541780
; Patent No. 5935831
; GENERAL INFORMATION:
; APPLICANT: Quax, Wilhelmus J.
; APPLICANT: Misset, Onno
; APPLICANT: Van der Laan, Jan M.
; APPLICANT: Lenting, Herman B.M.
; TITLE OF INVENTION: Mutated beta-lactam acylase genes
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,780
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/731,157
; FILING DATE:

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; APPLICATION NUMBER: EP 90200962
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER PH.D., BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: GBRO-027/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-494-7622
; TELEFAX: 415-857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2163 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas species
; STRAIN: SY77
; FEATURE:
; NAME/KEY: CDS
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; IDENTIFICATION METHOD: experimental
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US-08-541-780-1

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## Alignment Scores:

Pred. No.:	3.68e-11	Length:	2163
Score:	124.00	Matches:	27
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Best Local Similarity:	100.0%	Mismatches:	0
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US-10-568-337-2 (1-27) x US-08-541-780-1 (1-2163)

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Qy      1 MetLeuArgValLeuHisArgAlaAlaSerAlaLeuValMetAlaThrValIleGlyLeu 20
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Db      1 ATGCTGAGAGTTCTGCACCGGGCGGCGTCCGCCTTGTTATGGCGACTGTGATCGGCCTT 60

Qy      21 AlaProAlaValAlaPheAla 27
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# SCORE Search Results Details for Application 10568337 and Search Result 20071128\_153802\_us-10-568-337-5.rng.

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GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2007, 00:22:26 ; Search time 646 Seconds  
(without alignments)  
1147.147 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
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Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

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Post-processing: Minimum Match 0%  
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15: geneseqn2006s:\*

16: geneseqn2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
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	2	100	100.0	209	14	ADY34486	Ady34486 Pseudomon
	3	100	100.0	315	14	ADY34493	Ady34493 Pseudomon
	4	100	100.0	315	14	ADX70106	Adx70106 Recombina
	5	100	100.0	807	14	ADY34499	Ady34499 Human int
	6	100	100.0	807	14	ADX70111	Adx70111 Recombina
	7	94.8	94.8	101	4	AAH27732	Aah27732 GL7ACA (a
	8	94.8	94.8	101	5	AAH27740	Aah27740 Gl-7ACA r
	9	93.2	93.2	2482	4	AAI64747	Aai64747 Pseudomon
c	10	30.6	30.6	489	12	ADQ21106	Adq21106 Human sof
c	11	30.6	30.6	560	6	ABK35222	Abk35222 Human cDN
c	12	30.6	30.6	2222	10	ADL25751	Adl25751 Human can
c	13	30.6	30.6	2222	10	ADL25753	Adl25753 Human can
c	14	30.6	30.6	4369	12	ADQ25015	Adq25015 Human sof
c	15	29.6	29.6	1032	5	AAH74579	Aah74579 Nucleotid
	16	29	29.0	110000	4	AAI99682_19	Continuation (20 o
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c	18	28.6	28.6	46235	15	AEF73891	Aef73891 Human cor
c	19	28.6	28.6	49999	2	AAZ23903	Aaz23903 Human LOB
	20	28.2	28.2	706	2	ADR02076	Adr02076 A. gossyp
	21	28.2	28.2	1329	8	ACA19622	Aca19622 Prokaryot
c	22	27.6	27.6	346	3	AAA31766	Aaa31766 Plant mic
c	23	27.6	27.6	438	3	AAA31518	Aaa31518 Plant mic
	24	27.4	27.4	193303	12	ADF13122	Adf13122 Hypermeth
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	27	27.4	27.4	193303	12	ADI37261	Adi37261 Hypermeth
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c	29	27.2	27.2	8303	4	ABL05390	Abl05390 Drosophil
	30	27	27.0	1260	11	ACL26209	Acl26209 Rice abio
c	31	27	27.0	1387	13	ADX62879	Adx62879 Plant ful
	32	26.8	26.8	825	14	ACL70964	Acl70964 M. xanthu
c	33	26.8	26.8	2955	13	ADO84038	Ado84038 Plant ful
	34	26.8	26.8	10916	14	ACL64594	Acl64594 M. xanthu
c	35	26.8	26.8	33126	12	ADQ97546	Adq97546 Mouse can
c	36	26.6	26.6	441	11	ABD05702	Abd05702 Pseudomon
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c	39	26.6	26.6	3406	2	AAX20567	Aax20567 Polynucle
	40	26.4	26.4	494	14	ACL55838	Acl55838 Human col
	41	26.4	26.4	500	6	ABL65055	Abl65055 Lung canc
c	42	26.4	26.4	1441	11	AEA90319	Aea90319 Human NOV
c	43	26.4	26.4	2331	6	ABK34734	Abk34734 Human cDN
	44	26.4	26.4	3707	2	AAQ82792	Aaq82792 TRK1 gene
	45	26.4	26.4	3708	5	AAH21448	Aah21448 S. cerevi



&lt;!--StartFragment--&gt;RESULT 4

ADX70106

ID ADX70106 standard; DNA; 315 BP.

XX

AC ADX70106;

XX

DT 05-MAY-2005 (first entry)

XX

DE Recombinant protein preparation method-related gac1ss gene region SeqID8.

XX

KW fermentation; expression; recombinant protein; protein production;

KW interferon alpha 2; gene; ds.

XX

OS Brevundimonas diminuta.

XX

PN WO2005017174-A2.

XX

PD 24-FEB-2005.

XX

PF 12-AUG-2004; 2004WO-EP009055.

XX

PR 13-AUG-2003; 2003US-0494915P.

XX

PA (SANO ) SANDOZ AG.

XX

PI Stempfer G, Alliger P, Palma N;

XX

DR WPI; 2005-182386/19.

XX

PT Preparing recombinant polypeptides of interest, for producing large  
 PT variety of polypeptides of interest, by fermenting prokaryotic host cell  
 PT comprising a periplasm transformed with a recombinant expression system.

XX

PS Example 1; SEQ ID NO 8; 29pp; English.

XX

CC This invention relates to a novel method of preparing a recombinant  
 CC polypeptide of interest which comprises fermenting a prokaryotic host  
 CC cell comprising a periplasm transformed with a recombinant expression  
 CC system capable of bringing secretion of a polypeptide of interest into  
 CC the periplasm of the host cell and extracting the polypeptide of interest  
 CC from the periplasm. The method is useful for preparing a wide variety of  
 CC recombinant polypeptides of interest such as human interferon alpha 2.  
 CC The present sequence is that of a region of the B diminuta gac1ss gene  
 CC which was used in the exemplification of the invention.

XX

SQ Sequence 315 BP; 55 A; 86 C; 113 G; 61 T; 0 U; 0 Other;

Query Match 100.0%; Score 100; DB 14; Length 315;

Best Local Similarity 100.0%; Pred. No. 6.9e-23;

Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCCTGGTTCGTACGCGCCGCCTACAAGTGGTGATCTAGGGGAACGTTCCGGGGGCGTCG 60  
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 Db 116 ATCCTGGTTCGTACGCGCCGCCTACAAGTGGTGATCTAGGGGAACGTTCCGGGGGCGTCG 175

Qy 61 CTGCAACGGCGTCTCCGGATCTGGGTGAGAGGGGAAATCC 100  
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 Db 176 CTGCAACGGCGTCTCCGGATCTGGGTGAGAGGGGAAATCC 215

RESULT 5

ADY34499

ID ADY34499 standard; cDNA; 807 BP.

XX

AC ADY34499;

XX

DT 05-MAY-2005 (first entry)

XX

DE Human interferon-alpha 2B expression construct.

XX

KW Recombinant protein; interferon-alpha; mutant; gac gene; signal peptide;  
KW gene; ss.

XX

OS Homo sapiens.

OS Brevundimonas diminuta.

OS Chimeric.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 210..788

FT /\*tag= b

FT sig\_peptide 210..290

FT /\*tag= a

FT /note= "Gac gene signal sequence"

FT mat\_peptide 291..785

FT /\*tag= c

FT /product= "Human mature interferon-alpha 2B"

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PN WO2005017162-A2.

XX

PD 24-FEB-2005.

XX

PF 12-AUG-2004; 2004WO-EP009067.

XX

PR 13-AUG-2003; 2003US-0494914P.

XX

PA (SANO ) SANDOZ AG.

XX

PI Windisch J, Schoergendorfer K, Palma N, Knauseder F, Boehling H;

XX

DR WPI; 2005-182378/19.

DR P-PSDB; ADY34498.

XX

PT New expression vector comprising a polynucleotide encoding a fusion  
PT protein comprising the signal sequence of the gac gene of Pseudomonas  
PT diminuta and a polypeptide other than gac, useful for producing  
PT polypeptides.

XX

PS Example 1; SEQ ID NO 19; 39pp; English.

XX

CC The invention provides a process for the efficient and direct production  
 CC of a mature recombinant polypeptide in a prokaryotic host cell. A claimed  
 CC expression vector comprises a polynucleotide encoding a fusion protein  
 CC consisting of the signal sequence ADY34482 of the glutaryl 7-  
 CC aminocephalosporic acid acylase (gac) gene of Pseudomonas diminuta and  
 CC the polypeptide of interest. A prokaryotic host cell transformed with the  
 CC vector is cultured under conditions which cause expression of the  
 CC polynucleotide. Upon formation of the fusion protein, the signal sequence  
 CC is cleaved off and the polypeptide of interest is released into the  
 CC periplasm of the host cell. The expression vector is a plasmid,  
 CC preferably a high copy plasmid. The vector further comprises a  
 CC polynucleotide comprising the promoter region and the ribosomal binding

XX

2

12

— 11 —